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Research Article

Morphological and phylogenetic evidence reveal two new *Pseudohydnum* (*Auriculariales*, *Basidiomycota*) species from Guangxi and Xizang, China

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Abstract

Pseudohydnum (*Auriculariales*) is characterized by gelatinous, hydnoid basidiomata and longitudinally septate basidia. Currently, 26 species and one subspecies are accepted worldwide with molecular evidence, including two new species described here. In this study, specimens from Guangxi, Xizang, and Jilin provinces, China, were examined using morphological and phylogenetic analyses based on ITS1–5.8S–ITS2–nLSU sequences. The phylogeny resolves the genus as a well-supported monophyletic group. *Pseudohydnum umbrosum* is newly recorded from China. Two new species are described and illustrated as *P. fusiformis* from Xizang, characterized by olivaceous buff to clay-pink basidiomata, association with *Abies* at high elevations (above 3200 m), and the presence of fusiform cystidia—a feature previously known only from *P. cystidiatum* within the genus; and *P. rhododendri* from Guangxi, characterized by shell-shaped basidiomata with a pale mouse-gray pileal surface, the presence of cystidioles, and growing on living *Rhododendron*. The discovery of these new taxa and the new record further highlight China as a significant diversity center for *Pseudohydnum*.

Key words: *Auriculariales*, China, jelly fungi, new species, phylogeny, taxonomy

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Introduction

Pseudohydnum P. Karst. was established by Karsten with *P. gelatinosum* (Scop.) P. Karst. as the type species (Karsten 1868). The genus is characterized by gelatinous, laterally stipitate basidiomata with a hydnoid hymenophore, longitudinally septate phragmobasidia, and smooth, subglobose to ellipsoid basidiospores (Karsten 1868; Lowy 1971; Chen et al. 2020; Zhou et al. 2022, 2023). These distinctive features easily distinguish *Pseudohydnum* from other genera in *Auriculariales*, such as *Auricularia* Bull. (gelatinous, resupinate to substipitate basidiomata with hairs, transversely septate basidia); *Eichleriella* Bres. (leathery to ceraceous, cupulate to resupinate basidiomata with a smooth hymenophore); and *Exidia* Fr. (gelatinous basidiomata, allantoid basidiospores; Malysheva and Spirin 2017; Spirin et al. 2019a; Wu et al. 2021).

The genus was traditionally addressed in *Tremellales* due to its longitudinally septate basidia (Karsten 1868; Breitenbach and Kränzlin 1986). However, Bandoni (1984) redefined the concept of *Auriculariales* based on micromorphological, ultrastructural, ecological, and developmental data and suggested that *Pseudohydnum* belongs to this order. Subsequent phylogenetic studies have confirmed this placement, although the exact position of the genus within *Auriculariales* remains ambiguous (Weiß and Oberwinkler 2001; Malysheva and Spirin 2017; Spirin et al. 2019c, 2025). The presence of hydnoid basidiomata in *Pseudohydnum* indicates a distinctive classification status within *Auriculariales*, as taxa with diverse basidiomata morphologies, including jelly, stereoid, corticioid, hydnoid, and poroid forms, are not typically grouped together in the same order (Malysheva and Spirin 2017; Spirin et al. 2019c; Wu et al. 2021).

Recent taxonomic revisions and extensive field collections have substantially increased knowledge on the diversity of *Pseudohydnum*. Currently, 25 taxa, including 24 species and one subspecies with molecular evidence, are accepted in the genus, distributed across Asia, Europe, North America, South America, and Oceania, with no representatives yet documented from Africa (Karsten 1868; Breitenbach and Kränzlin 1986; Niveiro and Popoff 2011; Chen et al. 2020; Zhou et al. 2022, 2023; Spirin et al. 2023; Coelho-Nascimento et al. 2024; Lei et al. 2025; Wang et al. 2025b; Spirin et al. 2025). China, with its diverse forest ecosystems, is recognized as a significant biodiversity hotspot for macrofungi (Dai et al. 2010; Chen et al. 2015; Wu et al. 2019; Wang et al. 2023, 2024, 2025a, 2025b; Dong et al. 2024; Liu et al. 2025; Song et al. 2025; Yang et al. 2025; Zhao et al. 2025). Among them, 18 species have been recorded from Asia, including 17 species from China, highlighting the region as a significant diversity center for the genus. These Asian species are *P. abietinum* H.M. Zhou & Jing Si (Gansu of China), *P. brunneiceps* Y.L. Chen et al. (Jiangxi of China), *P. cystidiatum* Malysheva & V. Dudka (Yunnan of China, Vietnam), *P. himalayanum* Y.C. Dai et al. (Yunnan, Xizang of China), *P. laricicola* Zhu L. Yang et al. (Sichuan of China), *P. meridianum* Malysheva & Spirin (Yunnan of China, Vietnam), *P. motuoense* L. Lei & Q. Zhao (Xizang of China), *P. placibile* Malysheva & V. Dudka (Vietnam), *P. purum* L. Lei & Q. Zhao (Xizang of China), *P. sinobisporum* T. Bau et al. (Jilin, Heilongjiang of China), *P. sinogelatinosum* Y.C. Dai et al. (Yunnan, Sichuan, Xizang of China), *P. sororium* Zhu L. Yang & Q. Cai (Yunnan of China), *P. translucens* Lloyd (Jilin of China, Japan, Siberia, Russia Far East), and *P. umbrosum* Malysheva & Spirin (Russia Far East, also reported from Jilin of China in this study), as well as the type species *P. gelatinosum* (Scop.) P. Karst. (Inner Mongolia of China, Chen et al. 2020; Zhou et al. 2022, 2023; Spirin et al. 2023; Lei et al. 2025; Wang et al. 2025b). Notably, *P. gelatinosum* occurs in both Europe and Asia, representing a widespread Eurasian taxon, whereas *P. alienum* Spirin & Malysheva is so far found in Europe and the Caucasus region (Finland, Georgia, and the Russian Caucasus; Spirin et al. 2023).

The type species, *Pseudohydnum gelatinosum*, originally described from Croatia, has a wide distribution in Europe (Karsten 1868; Wojewoda 1981) and has also been reported from Asia (China) and North America (Zhou et al. 2022; Spirin et al. 2023). In the Caribbean, the species has been recorded from Jamaica, Puerto Rico, and recently from Cuba (Lowy 1971; Minter et al. 2001; Castro Hernández et al. 2022). In North America, in addition to *P. gelatinosum* s. str., one subspecies, *P. gelatinosum* subsp. *pusillum* (Ellis & Everh.) Miettinen & Viner,

and another species, *P. omnipavum* Spirin & Miettinen, have been documented (Spirin et al. 2023). South America, particularly the Brazilian Atlantic Forest, harbors four endemic species: *P. brasiliense* C.C. Nascim. et al., *P. brunneovelutinum* C.C. Nascim. & Menolli, *P. cupulisnymphae* C.C. Nascim. & Menolli, and *P. viridimontanum* C.C. Nascim. & Menolli (Coelho-Nascimento et al. 2024). Oceania harbors three endemic species: *P. orbiculare* J.A. Cooper, *P. tasmanicum* Y.C. Dai & G.M. Gates, and *P. totarae* (Lloyd) J.A. Cooper (Zhou et al. 2022).

While studying specimens of jelly fungi collected from China, several interesting taxa were identified. Among them, *Pseudohydnum umbrosum*, previously described from the Russian Far East, was discovered as a new record for the country. Additionally, two unknown taxa, morphologically distinct from all previously described species, were collected from Guangxi and Xizang provinces. In this study, phylogenetic analyses were performed based on the internal transcribed spacer (ITS1–5.8S–ITS2) and large subunit nuclear ribosomal RNA gene (nLSU) sequences to determine their phylogenetic positions. Combining morphological and molecular evidence, two new species, *Pseudohydnum fusiformis* from Xizang and *P. rhododendri* from Guangxi, are described and illustrated.

Materials and methods

Morphological studies

The specimens used in this study are deposited at the Fungarium of the State Key Laboratory of Efficient Production of Forest Resources, Beijing Forestry University, China (**BJFC**), and the Herbarium of Cryptogams at the Kunming Institute of Botany, Chinese Academy of Sciences, China (**KUN-HKAS**). Samples were photographed *in situ*, and important macro-morphological features were recorded. Morphological studies followed Wang et al. (2025a) and Zhou et al. (2022, 2023). Color terms follow Anonymous (1969) and Petersen (1996). Hand-cut sections of basidiomata were first treated with 5% KOH for a few minutes and then with 1% phloxine B ($C_{20}H_4Br_4Cl_2K_2O_5$). Micromorphological characters were examined with a Nikon Digital Sight DS-L3 or Leica ICC50 HD camera at magnifications up to 1000 times. At least 30 basidiospores per specimen were measured. For presentation of the size variation, 5% of the measurements were excluded from each end of the range and are provided in parentheses. Stalks were excluded for basidia measurement, and the hilar appendages were excluded for basidiospore measurement. The following abbreviations were used: **IKI** = Melzer's reagent, **IKI–** = neither amyloid nor dextrinoid, **CB** = Cotton Blue, **CB–** = acyanophilous in Cotton Blue, ***L*** = arithmetic average length of all measured spores, ***W*** = arithmetic average of all measured spore widths, ***Q*** = *L*/*W* ratios among the studied specimens, and ***n* (*a*/*b*)** = number of spores (*a*) measured from a given number of specimens (*b*).

Molecular studies and phylogenetic analysis

Genomic DNA was extracted from dried basidiomata using the CTAB plant genomic DNA extraction kit DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) following the manufacturer's guidelines with some modifications (Fan et al. 2021;

Zhou et al. 2022). The ITS1–5.8S–ITS2 region was amplified using the primer pairs ITS4 and ITS5, and the nLSU region was amplified using the primer pairs LROR and LR7 (White et al. 1990; Hopple and Vilgalys 1994). The PCR procedures for the ITS1–5.8S–ITS2 and nLSU regions followed Zhou et al. (2023). All newly generated sequences were submitted to GenBank and are listed in Table 1.

Sequences generated for this study and additional sequences downloaded from GenBank were partitioned into ITS1, 5.8S, ITS2, and nrLSU and then aligned separately using MAFFT v.74 (http://mafft.cbrc.jp/alignment/server/; Katoh et al. 2017) with the G-INS-i iterative refinement algorithm. Following manual optimization in BioEdit 7.0.5.3 (Hall 1999), the separate alignments were concatenated with Mesquite v.4.02 software (Maddison and Maddison 2025). The combined ITS1–5.8S–ITS2–nLSU dataset was analyzed to determine the phylogeny of *Pseudohydnum*, and sequences of *Protomerulius substuppeus* (Berk. & Cooke) Ryvarden and *Protomerulius subreflexus* (Lloyd) O. Miettinen & Ryvarden were used as outgroups following Zhou et al. (2022, 2023). The resulting alignment was deposited at TreeBase (submission ID 32526; Reviewer access URL: http://purl.org/phylo/treebase/phylows/study/TB2:S32526?x-access-code=70391994d471bfdc00e3cfdad510d1d5&format=html). Maximum likelihood (ML) and Bayesian inference (BI) methods were used for the phylogenetic analysis. ModelFinder v.2.2.0 with the corrected Akaike information criterion (AICc) was applied to estimate the best-fit partition scheme and evolutionary model for BI and ML analyses (Kalyaanamoorthy et al. 2017).

Maximum likelihood (ML) analysis was performed in RAxML v.8.2.12 (Stamatakis 2014) using the Cipres Science Gateway (http://www.phylo.org/portal2; Miller et al. 2010). All parameters in the ML analysis used default settings, and statistical support values were obtained using rapid bootstrapping with 1000 replicates.

Bayesian inference (BI) analysis was run with four chains for two independent runs and performed for two million generations, sampling every 1000 generations in MrBayes v.3.2.7 (Ronquist et al. 2012), until the split deviation frequency value was less than 0.01. The first 25% of the sampled trees were discarded as burn-in, and the remaining trees were used to reconstruct a majority-rule consensus and calculate BPP of the clades.

Trees were viewed in FigTree v.1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/, Rambaut 2018). Branches that received bootstrap support for ML and Bayesian posterior probabilities (BPP) greater than or equal to 70% (ML) and 0.90 (BPP) were considered to be significantly supported, following previous studies (Zhou et al. 2022; Lei et al. 2025).

Results

BLAST analysis of ITS sequences for the new species

BLAST searches of the ITS sequences of the holotype specimens against the GenBank database showed that the sequence of *P. rhododendri* (Cui 14495) was most similar to the type sequence of *P. placibile* (NR_198211.1), with 89.98% identity (100% query cover). The sequence of *P. fusiformis* (Dai 23556) was most similar to *P. omnipavum* (OM451499.1), with 97.04% identity (100% query cover). These low to moderate similarity values (89.98–97.04%) support the recognition of the two isolates as distinct species from their closest relatives.

Table 1. Taxa information and GenBank accession numbers of the sequences used in this study.

Species name	Samples	Locality	ITS no.	nLSU no.	References
Protomerulius subreflexus	OM 14402.1	Indonesia	MG757508	MG757508	Spirin et al. 2019b
P. substuppeus	O 19171	Costa Rica	JX134482	JQ764649	Spirin et al. 2019b
Pseudohydnum abietinum	Dai 24185*	China: Gansu	OP965350	OP965370	Zhou et al. 2023
P. abietinum	Dai 24194	China: Gansu	OP965351	OP965371	Zhou et al. 2023
P. alienum	Kotiranta 22407*	Finland	OM451494	OM451435	Spirin et al. 2023
P. alienum	LE 253853	Russia	OM451493	OM451430	Spirin et al. 2023
P. brasiliense	MPD570*	Brazil	OR625545	OR625561	Coelho-Nascimento et al. 2024
P. brasiliense	MPD572	Brazil	OR625546	OR625562	Coelho-Nascimento et al. 2024
P. brunneiceps	JXSB 0967*	China: Jiangxi	MN497254	MN497259	Chen et al. 2020
P. brunneiceps	JXSB0967-1	China: Jiangxi	MN497255	MN497260	Chen et al. 2020
P. brunneovelutinum	AGS118/2022	Brazil	OR625541	OR625557	Coelho-Nascimento et al. 2024
P. brunneovelutinum	NCC182	Brazil	OR625547	OR625563	Coelho-Nascimento et al. 2024
P. cupulisnymphae	NCC229	Brazil	OR625548	OR625564	Coelho-Nascimento et al. 2024
P. cupulisnymphae	NMJ420*	Brazil	OR625556	OR625570	Coelho-Nascimento et al. 2024
P. cystidiatum	HKAS 137494	China: Yunnan	PQ871457	PV276931	Wang et al. 2025b
P. cystidiatum	LE 313656*	Vietnam	OM451503	OM451463	Spirin et al. 2023
P. cystidiatum	LE 313657	Vietnam	OM451502	OM451464	Spirin et al. 2023
P. fusiformis	**Cui 12214**	**China: Xizang**	**PZ043114**	-	This study
P. fusiformis	**Dai 23556***	**China: Xizang**	**PZ043115**	**PZ043120**	This study
P. fusiformis	**WHM5603**	**China: Xizang**	**PZ043116**	-	This study
P. gelatinosum	Dai 21665	China: Inner Mongolia	ON243826	ON243924	Zhou et al. 2022
P. gelatinosum	Spirin 13369	Slovenia	OM451472	OM451434	Spirin et al. 2023
P. gelatinosum	LE 313661	Russia	OM451469	OM451466	Spirin et al. 2023
P. gelatinosum ssp. *pusillum*	Miettinen 16894	USA	ON117832	-	Spirin et al. 2023
P. gelatinosum ssp. *pusillum*	Miettinen 18987.2*	USA	ON117833	-	Spirin et al. 2023
P. gelatinosum ssp. *pusillum*	Miettinen 19625.1	USA	ON117834	ON117839	Spirin et al. 2023
P. himalayanum	Cui 17045*	China: Yunnan	ON243829	ON243927	Zhou et al. 2022
P. himalayanum	Cui 17065	China: Yunnan	ON243830	ON243928	Zhou et al. 2022
P. laricicola	HKAS 103433*	China: Sichuan	PQ871449	PV650295	Wang et al. 2025b
P. laricicola	HKAS 103450	China: Sichuan	PQ871450	PV276933	Wang et al. 2025b
P. meridianum	HKAS 145328	China: Yunnan	PQ871458	PQ877881	Wang et al. 2025b
P. meridianum	HKAS 145329	China: Yunnan	PV650322	PQ877882	Wang et al. 2025b
P. meridianum	LE 313568*	Vietnam	OM451501	OM451452	Spirin et al. 2023
P. motuoense	HKAS 134347*	China: Xizang	PP999440	PP998493	Lei et al. 2025
P. motuoense	HKAS 134348	China: Xizang	PP999439	PP998492	Lei et al. 2025
P. omnipavum	Miettinen 18877	USA	ON117836	OM451460	Spirin et al. 2023
P. omnipavum	Spirin 8667*	USA	OM451499	OM451441	Spirin et al. 2023
P. orbiculare	PDD 112653*	New Zealand	ON243831	ON243929	Zhou et al. 2022
P. orbiculare	PDD 112654	New Zealand	ON243832	-	Zhou et al. 2022
P. placibile	LE 313658*	Vietnam	OM451505	OM451465	Spirin et al. 2023
P. placibile	LE 313659	Vietnam	OM451504	OM451462	Spirin et al. 2023
P. purum	HKAS 134352*	China: Xizang	PP999437	PP998490	Lei et al. 2025
P. purum	HKAS 134353	China: Xizang	PP999438	PP998491	Lei et al. 2025
P. rhododendri	**Cui 14495***	**China: Guangxi**	**PZ043112**	**PZ043118**	This study
P. rhododendri	**Cui 14496**	**China: Guangxi**	**PZ043113**	**PZ043119**	This study
P. sinobisporum	HMJAU 33728	China: Heilongjiang	OP965349	OP965369	Zhou et al. 2023

Species name	Samples	Locality	ITS no.	nLSU no.	References
P. sinobisporum	SYL 2307*	China: Jilin	OP965348	OP965368	Zhou et al. 2023
P. sinogelatinosum	Cui 17074	China: Yunnan	ON243834	ON243930	Zhou et al. 2022
P. sinogelatinosum	Dai 23017*	China: Yunnan	ON243836	ON243932	Zhou et al. 2022
P. sororium	HKAS 108870*	China: Yunnan	PQ871453	PQ877885	Wang et al. 2025b
P. sororium	HKAS 145330	China: Yunnan	PQ871454	PQ877886	Wang et al. 2025b
P. sororium	HKAS 145331	China: Yunnan	PQ871455	PQ877887	Wang et al. 2025b
P. tasmanicum	Cui 16721*	Australia	ON243838	ON243934	Zhou et al. 2022
P. tasmanicum	Dai 18724	Australia	ON243839	ON243935	Zhou et al. 2022
P. totarae	PDD 112652	New Zealand	ON243841	-	Zhou et al. 2022
P. totarae	PDD 112655	New Zealand	ON243842	ON243936	Zhou et al. 2022
P. translucens	Dai 23740	China: Jilin	OP965345	OP965365	Zhou et al. 2023
P. translucens	LE 313582	Russia	OM451498	OM451459	Spirin et al. 2023
P. translucens	LE 313586	Russia	OM451496	OM451455	Spirin et al. 2023
P. umbrosum	HMJAU6847	China: Jilin	**PZ043117**	**PZ043121**	This study
P. umbrosum	LE 312767*	Russia	OM451500	OM451453	Spirin et al. 2023
P. viridimontanum	NCC266*	Brazil	OR625552	OR957373	Coelho-Nascimento et al. 2024
P. viridimontanum	NCC273	Brazil	OR625553	OR957374	Coelho-Nascimento et al. 2024
Stypellopsis farlowii	GB Larsson 12337*	USA	NR_164269	MG857099	Spirin et al. 2019a
S. hyperborea	Spirin 11066 (O)	Norway	MG857096	MG857102	Spirin et al. 2019a

The new species and newly generated sequences are shown in bold. "*" indicating the holotype.

Phylogeny of *Pseudohydnum*

The combined ITS1–5.8S–ITS2–nLSU dataset contained 61 ITS and 55 nrLSU sequences from 61 specimens, representing 27 taxa and the outgroup (Table 1). For Bayesian inference (BI), ModelFinder suggested SYM+G4 as the best-fit model for ITS1, 5.8S, and ITS2, and GTR+F+I+G4 as the best-fit model for nrLSU. For maximum likelihood (ML), the best-fit models were GTR+F+G4 for ITS1, 5.8S, and ITS2, and GTR+F+I+G4 for nrLSU. The BI analysis generated a topology nearly identical to that obtained from the ML analysis, with an average standard deviation of split frequencies of 0.006406. Accordingly, only the ML tree is presented (Fig. 1), with ML bootstrap values (BS) ≥ 70% and Bayesian posterior probabilities (BPP) ≥ 0.90 shown on branches.

The ITS1–5.8S–ITS2–nLSU-based phylogeny showed that *Pseudohydnum* is a well-supported monophyletic group comprising 27 taxa (98% ML, 1 BPP; Fig. 1). Two new species, described in this study as *Pseudohydnum fusiformis* and *Pseudohydnum rhododendri*, were nested within *Pseudohydnum* but occupied distinct phylogenetic positions.

Three specimens of *Pseudohydnum fusiformis* from Xizang, southwestern China, formed a distinct and strongly supported lineage (100% ML, 0.99 BPP) that formed a small subclade with *P. omnipavum* (0.91 BPP; Fig. 1). Together with a well-supported subclade (98% ML, 1 BPP) comprising *P. alienum*, *P. himalayanum*, *P. laricicola*, *P. sinobisporum*, and *P. translucens*, they formed a large well-supported clade (99% ML, 1 BPP).

Two specimens of *Pseudohydnum rhododendri* from Guangxi, southern China, formed an independent and strongly supported lineage (100% ML, 1 BPP) within *Pseudohydnum*.

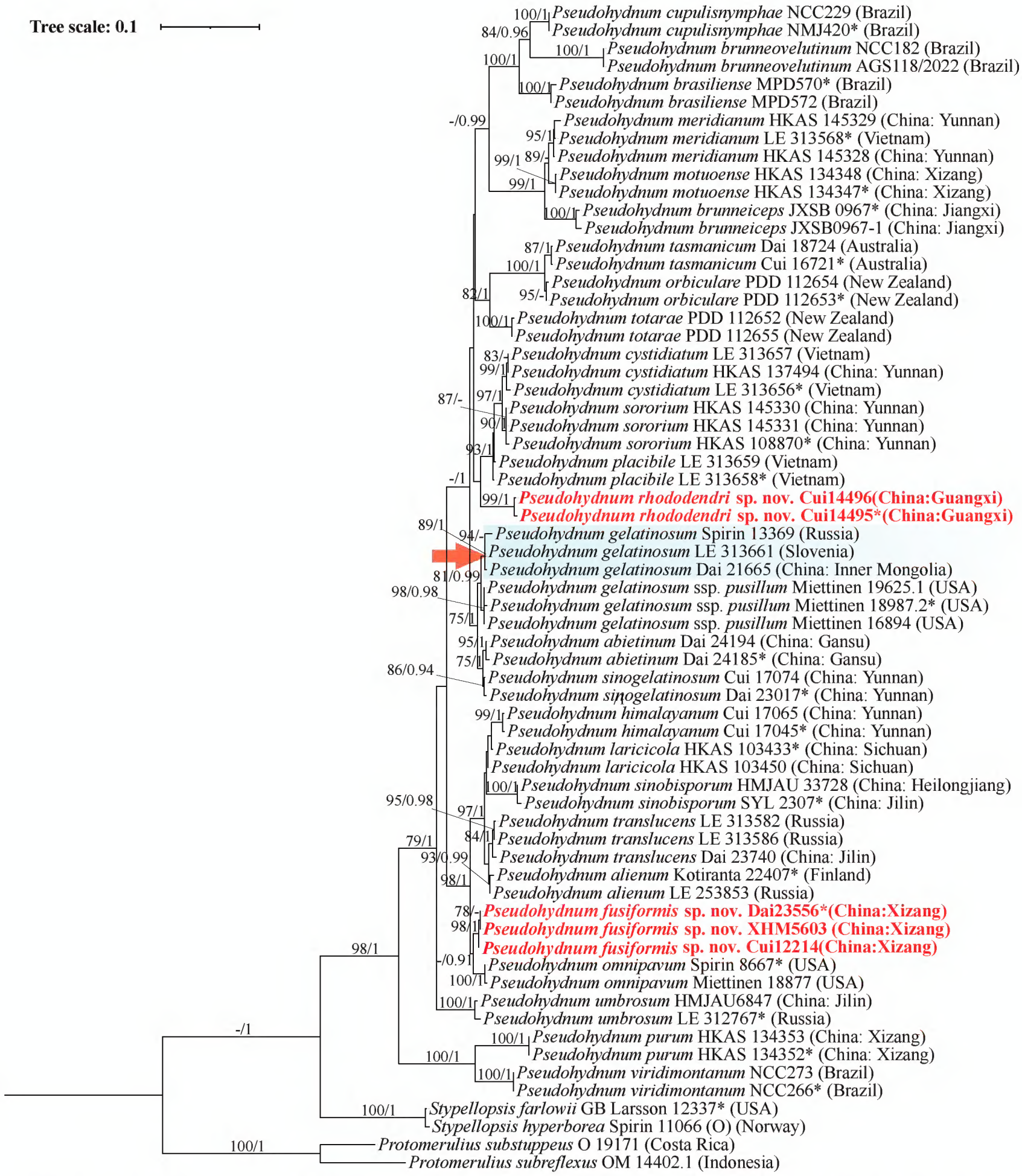
Tree scale: 0.1
Pseudohydnum cupulisnymphae NCC229 (Brazil)
Pseudohydnum cupulisnymphae NMJ420* (Brazil)
Pseudohydnum brunneovelutinum NCC182 (Brazil)
Pseudohydnum brunneovelutinum AGS118/2022 (Brazil)
Pseudohydnum brasiliense MPD570* (Brazil)
Pseudohydnum brasiliense MPD572 (Brazil)
Pseudohydnum meridianum HKAS 145329 (China: Yunnan)
Pseudohydnum meridianum LE 313568* (Vietnam)
Pseudohydnum meridianum HKAS 145328 (China: Yunnan)
Pseudohydnum motuoense HKAS 134348 (China: Xizang)
Pseudohydnum motuoense HKAS 134347* (China: Xizang)
Pseudohydnum brunneiceps JXSB 0967* (China: Jiangxi)
Pseudohydnum brunneiceps JXSB0967-1 (China: Jiangxi)
Pseudohydnum tasmanicum Dai 18724 (Australia)
Pseudohydnum tasmanicum Cui 16721* (Australia)
Pseudohydnum orbiculare PDD 112654 (New Zealand)
Pseudohydnum orbiculare PDD 112653* (New Zealand)
Pseudohydnum totarae PDD 112652 (New Zealand)
Pseudohydnum totarae PDD 112655 (New Zealand)
Pseudohydnum cystidiatum LE 313657 (Vietnam)
Pseudohydnum cystidiatum HKAS 137494 (China: Yunnan)
Pseudohydnum cystidiatum LE 313656* (Vietnam)
Pseudohydnum sororium HKAS 145330 (China: Yunnan)
Pseudohydnum sororium HKAS 145331 (China: Yunnan)
Pseudohydnum sororium HKAS 108870* (China: Yunnan)
Pseudohydnum placibile LE 313659 (Vietnam)
Pseudohydnum placibile LE 313658* (Vietnam)
Pseudohydnum rhododendri sp. nov. Cui14496(China:Guangxi)
Pseudohydnum rhododendri sp. nov. Cui14495*(China:Guangxi)
Pseudohydnum gelatinosum Spirin 13369 (Russia)
Pseudohydnum gelatinosum LE 313661 (Slovenia)
Pseudohydnum gelatinosum Dai 21665 (China: Inner Mongolia)
Pseudohydnum gelatinosum ssp. pusillum Miettinen 19625.1 (USA)
Pseudohydnum gelatinosum ssp. pusillum Miettinen 18987.2* (USA)
Pseudohydnum gelatinosum ssp. pusillum Miettinen 16894 (USA)
Pseudohydnum abietinum Dai 24194 (China: Gansu)
Pseudohydnum abietinum Dai 24185* (China: Gansu)
Pseudohydnum sinogelatinosum Cui 17074 (China: Yunnan)
Pseudohydnum sinogelatinosum Dai 23017* (China: Yunnan)
Pseudohydnum himalayanum Cui 17065 (China: Yunnan)
Pseudohydnum himalayanum Cui 17045* (China: Yunnan)
Pseudohydnum laricicola HKAS 103433* (China: Sichuan)
Pseudohydnum laricicola HKAS 103450 (China: Sichuan)
Pseudohydnum sinobisporum HMJAU 33728 (China: Heilongjiang)
Pseudohydnum sinobisporum SYL 2307* (China: Jilin)
Pseudohydnum translucens LE 313582 (Russia)
Pseudohydnum translucens LE 313586 (Russia)
Pseudohydnum translucens Dai 23740 (China: Jilin)
Pseudohydnum alienum Kotiranta 22407* (Finland)
Pseudohydnum alienum LE 253853 (Russia)
Pseudohydnum fusiformis sp. nov. Dai23556*(China:Xizang)
Pseudohydnum fusiformis sp. nov. XHM5603 (China:Xizang)
Pseudohydnum fusiformis sp. nov. Cui12214(China:Xizang)
Pseudohydnum omnipavum Spirin 8667* (USA)
Pseudohydnum omnipavum Miettinen 18877 (USA)
Pseudohydnum umbrosum HMJAU6847 (China: Jilin)
Pseudohydnum umbrosum LE 312767* (Russia)
Pseudohydnum purum HKAS 134353 (China: Xizang)
Pseudohydnum purum HKAS 134352* (China: Xizang)
Pseudohydnum viridimontanum NCC273 (Brazil)
Pseudohydnum viridimontanum NCC266* (Brazil)
Stypellopsis farlowii GB Larsson 12337* (USA)
Stypellopsis hyperborea Spirin 11066 (O) (Norway)
Protomerulius substuppeus O 19171 (Costa Rica)
Protomerulius subreflexus OM 14402.1 (Indonesia)

Figure 1. Maximum likelihood tree (ML) illustrating the phylogeny of *Pseudohydnum* based on a combined ITS1–5.8S–ITS2–nLSU dataset. Branches are labeled with ML bootstrap values (BS) higher than 70% and Bayesian posterior probabilities (BPP) higher than 0.90. New species are indicated in red bold with "sp. nov."; the type species is indicated by a red arrow; type specimens are indicated with an asterisk (*).

Taxonomy

***Pseudohydnum fusiformis* Xin Zhang & Y.C. Dai, sp. nov.**

MycoBank No: 862555

Fig. 2

Diagnosis. It is characterized by solitary basidiomata with a lateral stipe paler than pileal surface when fresh, the presence of fusiform cystidia, and growing on *Abies delavayi* var. *motuoensis* at high elevations (above 3200 m).

Holotype. CHINA • Xizang Autonomous Region, Linzhi, Bomi County, the road from Bomi to Motuo, on fallen trunk of *Abies delavayi* var. *motuoensis*, elev. 3500 m, 26 October 2021, Dai 23556 (BJFC038128, holotype).

Etymology. *Fusiformis* (Lat.): refers to the fusiform cystidia of the species.

Fruitbody. Basidiomata annual, gelatinous when fresh, brittle when dry, solitary, with a lateral stipe. Pilei irregular, projecting up to 2.4 cm, 1.8 cm wide and 2.2 mm thick when dry. Pileal surface olivaceous buff (4C4) to clay-pink (6D4) when fresh, become cigar brown (6F5) when dry. Spines white (1A1), paler than pileal surface, conical when fresh, cream (4A2) when dry, 2 per mm at base, up to 2 mm long when dry. Context translucent when fresh. Stipe translucent when fresh, up to 12 mm long and 3 mm in diam when dry.

Hyphal structure. Hyphal system monomitic; generative hyphae with clamp connections. Contextual hyphae hyaline, thin- to slightly thick-walled, frequently branched, interwoven, 2–6 μm in diam. Tramal hyphae hyaline, thin-walled, frequently branched, interwoven, 3–4 μm in diam. Cystidia fusiform, 19–50 × 2–6 μm; cystidioles absent. Hyphidia occasionally branched. Basidia four-celled, barrel-shaped, subglobose or globose, 10.5–12 × 10–11 μm; sterigmata up to 13 μm long and 2–3 μm in diam. Probasidia fusiform to lageniform, 10–15 × 6–9 μm. Basidiospores ovoid to broadly ellipsoid, hyaline, thin-walled, IKI–, CB–, (6.8–)7–8.5(–9) × (5.2–)5.5–7(–8) μm, *L* = 7.61 μm, *W* = 6.32 μm, *Q* = 1.19–1.22 (60/2).

Additional specimens examined (paratypes). CHINA • Xizang Autonomous Region, Motuo County, on fallen trunk of *Abies*, elev. 3400 m, 20 September 2014, Cui 12214 (BJFC017128); the road from Bomi to Motuo, elev. 3217 m, 22 August 2018, WXH 5603 (HKAS112529).

Pseudohydnum rhododendri **Xin Zhang & Y.C. Dai, sp. nov.**

MycoBank No: 862557

Fig. 3

Diagnosis. It is characterized by shell-shaped, pileate basidiomata with a rudimentary stipe and pale mouse-gray pileal surface when fresh, barrel-shaped to subglobose basidia, branched hyphidia, and growing on *Rhododendron*.

Holotype. CHINA • Guangxi Zhuang Autonomous Region, Guilin, Maoershan National Nature Reserve, on living tree of *Rhododendron thunbergii*, elev. 1732 m, 13 July 2017, Cui 14495 (holotype, BJFC029363).

Etymology. *Rhododendri* (Lat.): refers to the species growing on *Rhododendron*.

Fruitbody. Basidiomata annual, pileate with a rudimentary stipe, imbricate, gelatinous when fresh, brittle when dry. Pilei shell-shaped, projecting up to 1.2 cm, 2.1 cm wide and 1 mm thick at base when dry. Pileal surface pale mouse-gray (7C2) when fresh, become chestnut (7E7) when dry. Spines white (1A1) and conical when fresh, become buff (4A4) when dry, 4–6 per mm at base, up to 1 mm long. Context translucent when fresh.

Hyphal structure. Hyphal system monomitic; generative hyphae with clamp connections. Contextual hyphae hyaline, thin-walled, frequently branched, interwoven, 10–18 μm in diam. Tramal hyphae hyaline, thin-walled, occasionally branched, interwoven, 6–8.5 μm in diam. Cystidioles fusiform to lageniform,

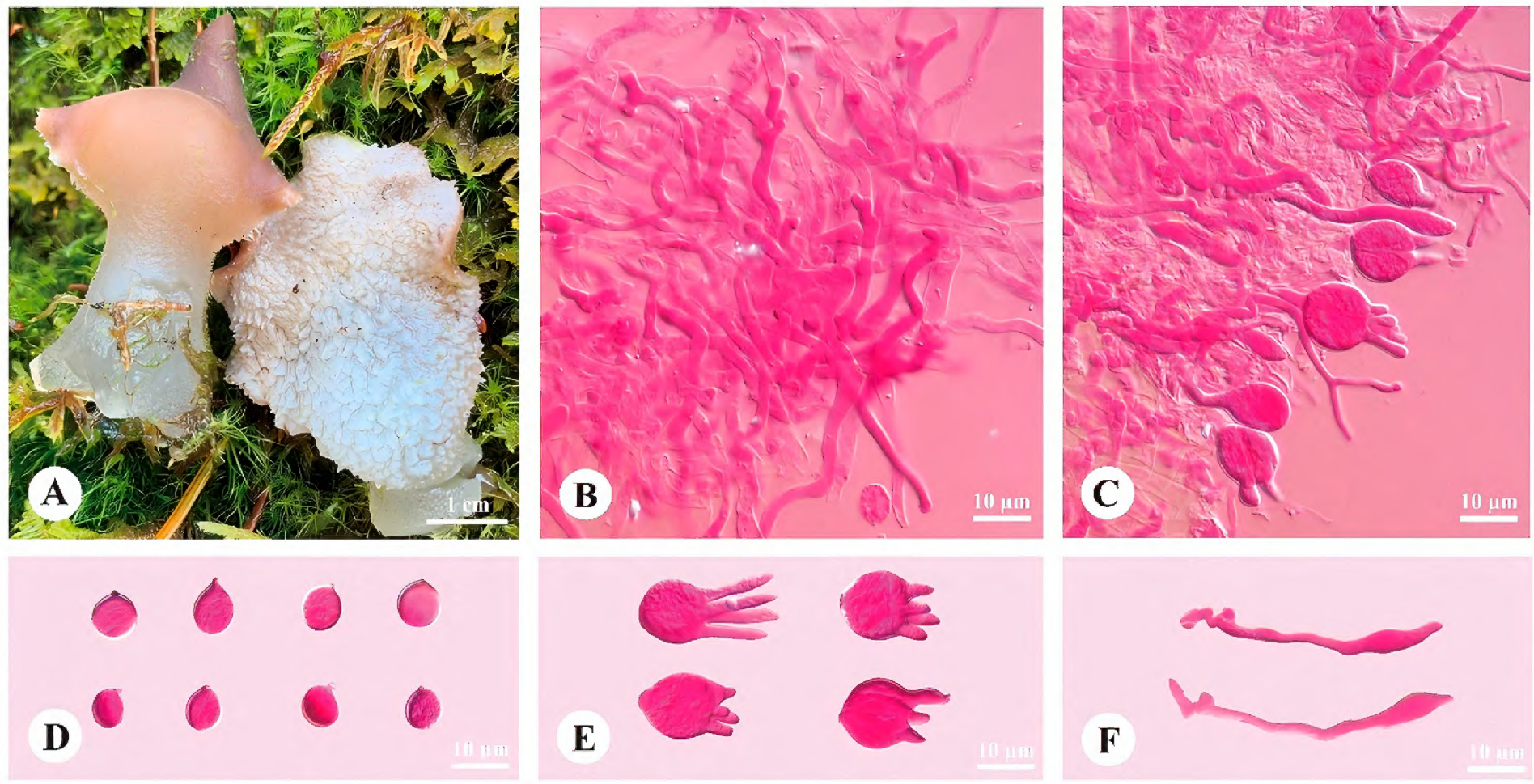

Figure 2. Basidiomata and microscopic structures of *Pseudohydnum fusiformis* (holotype, Dai 23556). **A.** Basidiomata; **B.** Tramal hyphae; **C.** A section of the hymenium; **D.** Basidiospores; **E.** Basidia; **F.** Cystidia.

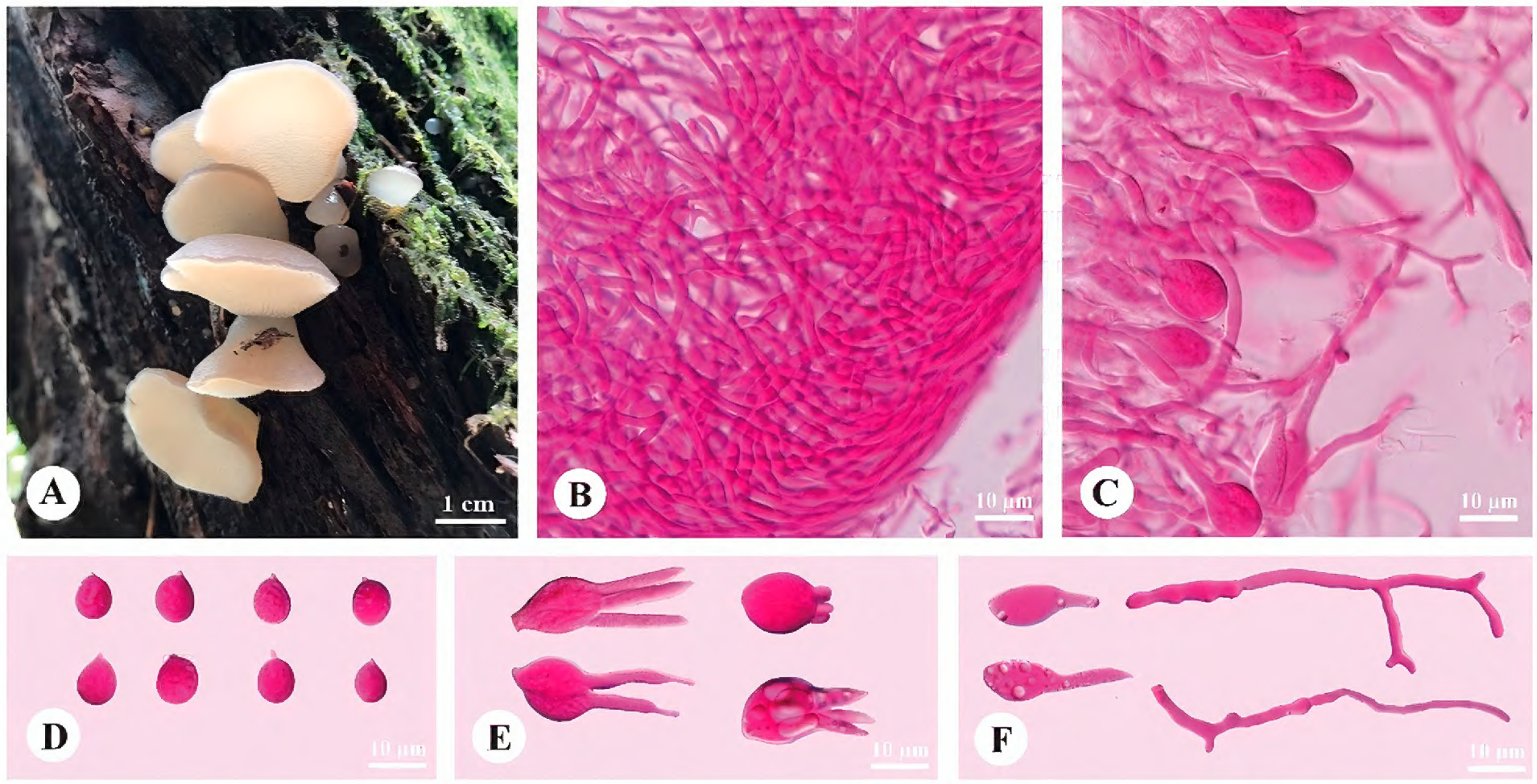

Figure 3. Basidiomata and microscopic structures of *Pseudohydnum rhododendri* (holotype, Cui 14495). **A.** Basidiomata; **B.** Tramal hyphae; **C.** A section of the hymenium; **D.** Basidiospores; **E.** Basidia; **F.** Cystidioles and hyphidia.

19–27 × 6–9 μm. Hyphidia occasionally branched. Basidia two- or four-celled, barrel-shaped, ovoid to subglobose, occasionally with guttules, 12–16 × 9.5–11.5 μm; sterigmata up to 16 μm long and 2–3.5 μm in diam. Basidiospores broadly ellipsoid to ovoid, hyaline, thin-walled, IKI–, CB–, (7–)7.5–9(–9.8) × 6–8(–8.8) μm, *L* = 8.2 μm, *W* = 6.96 μm, *Q* = 1.15–1.21 (60/2).

Additional specimen examined (paratype). China • Guangxi Zhuang Autonomous Region, Guilin, Maoershan National Nature Reserve, elev. 1750 m, on living tree of *Rhododendron thunbergii*, 13 July 2017, Cui 14495 (BJFC029364).

Discussion

Morphological examination and phylogenetic analysis identified 27 taxa of *Pseudohydnum* as a well-supported monophyletic group (98% ML, 1 BPP; Fig. 1), distributed across Asia, Europe, North and South America, and Oceania. In this study, two new species from Xizang and Guangxi, China, viz., *Pseudohydnum fusiformis* and *P. rhododendri*, are formally described based on morphological and phylogenetic evidence.

Pseudohydnum fusiformis was found at high elevations (> 3200 m) in Xizang, southwestern China, growing on fallen trunks of *Abies delavayi* var. *motuoensis*. Phylogenetically, it formed a small subclade with *P. omnipavum* (0.91 BPP; Fig. 1), but *P. omnipavum* differs from *P. fusiformis* in having a finely tomentose to strigose, watery-grayish pileal surface, shorter basidiospores (5.8–7.3 µm vs. 7–8.5 µm in length), and is distributed in North America (Spirin et al. 2023). This subclade belongs to a larger well-supported clade (99% ML, 1 BPP), which also includes another subclade (97% ML, 1 BPP) containing five Eurasian species (*P. alienum*, *P. himalayanum*, *P. laricicola*, *P. sinobisporum*, and *P. translucens*). This larger clade is characterized by species with predominantly pale-colored basidiomata and a frequent association with conifers, especially *Abies* (Zhou et al. 2022, 2023; Spirin et al. 2023; Wang et al. 2025b). Morphologically, *P. fusiformis* is most strikingly characterized by the presence of fusiform cystidia, a feature otherwise known only from *P. cystidiatum* within the genus. However, *P. cystidiatum* differs from *P. fusiformis* in having a rudimentary or sessile stipe, tapering, broader cystidia (15.5–16.7 µm vs. 2–6 µm in width), and growing on decayed wood in subtropical lowland forests of Vietnam and Yunnan, China, whereas *P. fusiformis* grows on *Abies* in high-elevation boreal forests (Spirin et al. 2023). Among the *Abies*-associated species, *P. himalayanum*, *P. abietinum*, and *P. sinogelatinosum* share a similar pinkish pileal surface with *P. fusiformis*, but they differ from *P. fusiformis* by having basidiospores with a large guttule; *P. abietinum* further differs by having a rudimentary stipe, and *P. himalayanum* and *P. sinogelatinosum* differ by having longer basidia (12–17.5 µm in *P. himalayanum* and 12–15 µm in *P. sinogelatinosum* vs. 10.5–12 µm in *P. fusiformis*; Zhou et al. 2022, 2023). Similarly, *P. alienum* and *P. translucens* differ from *P. fusiformis* by having a watery-grayish, strigose pileal surface and denser hymenial spines (6–8 per mm in *P. alienum* and *P. translucens* vs. 2 per mm in *P. fusiformis*; Spirin et al. 2023).

Pseudohydnum rhododendri was found in Guangxi, southern China, growing on living *Rhododendron thunbergii* in a montane forest (1732–1750 m elevation). Phylogenetically, it formed an independent lineage (100% ML, 1 BPP; Fig. 1) within *Pseudohydnum*. Morphologically, *P. alienum*, *P. cystidiatum*, *P. orbiculare*, *P. tasmanicum*, and *P. umbrosum* share a generally grayish pileal surface and a rudimentary or absent stipe with *P. rhododendri*. However, *P. alienum*, *P. cystidiatum*, and *P. orbiculare* differ from *P. rhododendri* in spine density (6–8 per mm in *P. alienum*, 3–4 per mm in *P. cystidiatum*, 0.5–1 per mm in *P. orbiculare* vs. 4–6 per mm in *P. rhododendri*) and consistently four-celled basidia (Zhou et al. 2022; Spirin et al. 2023). *P. umbrosum* shares a similar spine density with *P. rhododendri* but differs from *P. rhododendri* in having a dark brown to blackish pileal surface and occurring on conifers in Russia and

northeastern China (Spirin et al. 2023). *P. tasmanicum* resembles *P. rhododendri* by having two- to four-celled basidia and almost the same shape and size of basidiospores but differs by having simple hyphidia, sparser hymenial spines (2–3 per mm vs. 4–6 per mm), and growing on *Eucalyptus* and *Nothofagus* in Australia (Zhou et al. 2022). Most significantly, *P. rhododendri* is the only species in the genus that possesses cystidioles and is currently known from living *Rhododendron* in Guangxi, southern China—a highly specialized host association unprecedented in the genus and recorded here for the first time.

In conclusion, the discovery of *Pseudohydnum fusiformis* with fusiform cystidia—a feature previously known only from *P. cystidiatum*—and a high-elevation *Abies* habitat in Xizang and *P. rhododendri* with cystidioles, two- to four-celled basidia, and an unprecedented host association on living *Rhododendron* in Guangxi, southern China, together highlight the morphological and ecological diversity of *Pseudohydnum* in China. The morphological features observed (e.g., basidia type, presence of cystidia, host specificity) suggest that host associations may have played a role in species diversification within *Pseudohydnum*, but further studies are needed to test this hypothesis.

References

Anonymous (1969) Flora of British Fungi. Colour Identification Chart. Her Majesty's Stationery Office, London.

Bandoni RJ (1984) The *Tremellales* and *Auriculariales*: An alternative classification. Transactions of the Mycological Society of Japan 25: 489–530.

Breitenbach J, Kränzlin F (1986) Fungi of Switzerland. Volume 2: Non-gilled fungi, *Heterobasidiomycetes*, *Aphyllophorales*, *Gasteromycetes*. Verlag Mykologia, Lucerne.

Castro Hernández L, Camino Vilaró M, Abreu Herrera Y (2022) Primer registro del género *Pseudohydnum* (*Exidiaceae*, *Auriculariales*, *Basidiomycota*) para Cuba. Acta Botanica Mexicana 129: e1975. https://doi.org/10.21829/abm129.2022.1975

Chen JJ, Cui BK, Zhou LW, Korhonen K, Dai YC (2015) Phylogeny, divergence time estimation, and biogeography of the genus *Heterobasidion* (*Basidiomycota*, *Russulales*). Fungal Diversity 71: 185–200. https://doi.org/10.1007/s13225-014-0317-2

Chen YL, Su MS, Zhang LP, Zou Q, Wu F, Zeng NK, Liu M (2020) *Pseudohydnum brunneiceps* (*Auriculariales*, *Basidiomycota*), a new species from Central China. Phytotaxa 441: 87–94. https://doi.org/10.11646/phytotaxa.441.1.8

Coelho-Nascimento C, Zabin DA, Silva-Filho AGDS, Drewinski MP, Alves-Silva G, Kossmann T, Titton M, Drechsler-Santos ER, Menolli N (2024) Unraveling the cat's tongue mushrooms: Four new species of *Pseudohydnum* from Brazil based on morphological and molecular phylogenetic evidence. Mycologia 116(5): 792–820.

Dai YC (2010) A revised checklist of corticoid and hydroid fungi in China for 2010. Mycoscience 52: 69–79. https://doi.org/10.1007/S10267-010-0068-1

Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, Muhammad A, Zhao CL (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere 15(1): 1110–1293. https://doi.org/10.5943/mycosphere/15/1/10

Fan LF, Alvarenga RLM, Gibertoni TB, Wu F, Dai YC (2021) Four new species in the *Tremella fibulifera* complex (*Tremellales*, *Basidiomycota*). Mycokeys 82: 33–56. https://doi.org/10.3897/mycokeys.82.63241

Hall TA (1999) Bioedit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

Hopple JS, Vilgalys R (1994) Phylogenetic relationships among coprinoid taxa and allies based on data from restriction site mapping of nuclear rDNA. Mycologia 86: 96–107. https://doi.org/10.1080/00275514.1994.12026378

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods 14: 587–589. https://doi.org/10.1038/nmeth.4285

Karsten PA (1868) *Auriculariei*, *Clavariei* et *Tremellini*, in paroecia Tammela crescentes. Notiser ur Sällskapets pro Fauna et Flora Fennica Förhandlingar 9: 365–374.

Katoh K, Rozewicki J, Yamada KD (2017) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Lei L, Luangharn T, Yu FM, Zhao Q (2025) Two new species of *Pseudohydnum* (*Auriculariales*, *Basidiomycota*) from the Qinghai–Tibet Plateau in China. Phytotaxa 690(2): 243–254. https://doi.org/10.11646/phytotaxa.690.2.5

Liu LL, Ren YL, Habib K, Lu CT, Wu YP, Long SH, Lin Y, Zhang X, Kang YQ, Wijayawardene NN, Wang F, Elgorban AM, Al-Rejaie S, Samarakoon MC, Shen XC, Li QR (2025) New taxa of *Xylariales* from karst ecosystems in southwestern China. Mycosphere 16(1): 1–78. https://doi.org/10.5943/mycosphere/16/1/1

Lowy B (1971) *Tremellales*. Flora Neotropica 6: 1–153.

Maddison WP, Maddison DR (2025) Mesquite: A modular system for evolutionary analysis. Version 4.02. https://www.mesquiteproject.org

Malysheva V, Spirin V (2017) Taxonomy and phylogeny of the *Auriculariales* (*Agaricomycetes*, *Basidiomycota*) with stereoid basidiocarps. Fungal Biology 121: 689–715. https://doi.org/10.1016/j.funbio.2017.05.001

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES science gateway for inference of large phylogenetic trees. In: Proceedings of the Gateway Computing Environments Workshop (GCE), New Orleans, 1–8. https://doi.org/10.1109/GCE.2010.5676129

Minter DW, Rodríguez M, Mena J [Eds] (2001) Fungi of the Caribbean: An Annotated Checklist. UDMS Publishing, Glasgow.

Niveiro N, Popoff OF (2011) *Pseudohydnum gelatinosum* (*Tremellales*, *Basidiomycota*) in the Argentinean Yungas. Boletín de la Sociedad Argentina de Botánica 46: 223–226.

Petersen JH (1996) The Danish Mycological Society's Colour-Chart. Foreningen til Svampekundskabens Fremme, Greve.

Rambaut A (2018) FigTree v1.4.4, a graphical viewer of phylogenetic trees. University of Edinburgh, Edinburgh. http://tree.bio.ed.ac.uk/software/figtree/

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542. https://doi.org/10.1093/sysbio/sys029

Song CG, Xu TM, Xu YH, Wang D, Zeng L, Fan XP, Sun YF, Cui BK (2025) Systematic revision, molecular phylogeny and divergence times of *Thelephorales* (*Basidiomycota*). Mycosphere 16(1): 296–422. https://doi.org/10.5943/mycosphere/16/1/5

Spirin V, Malysheva V, Haelewaters D, Larsson KH (2019a) Studies in the *Stypella vermiformis* group (*Auriculariales*, *Basidiomycota*). Antonie van Leeuwenhoek 112: 753–764. https://doi.org/10.1007/s10482-018-01209-9

Spirin V, Malysheva V, Miettinen O, Vlasak J, Mendes Alvarenga RL, Gibertoni TB, Ryvarden L, Larsson KH (2019b) On *Protomerulius* and *Heterochaetella* (*Auriculariales*,

Basidiomycota). Mycological Progress 18(9): 1079–1099. https://doi.org/10.1007/s11557-019-01507-0

Spirin V, Malysheva V, Roberts P, Trichies G, Savchenko A, Larsson KH (2019c) A convolute diversity of the *Auriculariales* (*Agaricomycetes*, *Basidiomycota*) with sphaeropedunculate basidia. Nordic Journal of Botany 37(7): e02394. https://doi.org/10.1111/njb.02394

Spirin V, Malysheva V, Viner I, Dudka V, Grebenc T, Miettinen O (2023) Taxonomy and multigene phylogeny of *Pseudohydnum* (*Auriculariales*, *Basidiomycota*). Mycological Progress 22(40): 1–25. https://doi.org/10.1007/s11557-023-01895-4

Spirin V, Malysheva V, Viner I, Alvarenga RLM, Grebenc T, Gruhn G, Savchenko A, Grootmyers D, Ryvarden L, Vlasák J, Larsson K-H, Nilsson RH (2025) Additions to the taxonomy of the *Auriculariales* (*Basidiomycota*) with pedunculate basidia. MycoKeys 120: 339–392. https://doi.org/10.3897/mycokeys.120.155492

Stamatakis A (2014) RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30(9): 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Wang CG, Zhao H, Liu HG, Zeng GY, Yuan Y, Dai YC (2023) A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in *Irpicaceae* (*Polyporales*, *Basidiomycota*). Mycosphere 14(1): 1665–1729. https://doi.org/10.5943/mycosphere/14/1/19

Wang CG, Dai YC, Kout J, Gates GM, Liu HG, Yuan Y, Vlasák J (2024) Multi-gene phylogeny and taxonomy of *Physisporinus* (*Polyporales*, *Basidiomycota*). Mycosphere 15(1): 1455–1521. https://doi.org/10.5943/mycosphere/15/1/12

Wang CG, Wu YD, Zhang X, Dai YC, Li ZH, Yuan Y (2025a) Studies in phylogeny and divergence times of *Irpicaceae* and *Meripilaceae* (*Polyporales*, *Basidiomycota*), with an emphasis on *Ceriporia* and *Meripilus* including ten new species. IMA Fungus 16: e161336. https://doi.org/10.3897/imafungus.16.161336

Wang X-H, Cai Q, Yu F-M, Yang Z-L, Zhou S-Y, Wang Z-R, Cui Y-Y, Wang Y, Zhang P, Cao S-Q, Zhu X-T, Lei L, Lu J-R, Li J-N, Wang G-S, Jia L-K, Mu L-H, Li G-M, Li M-X, Yang B-Q, Feng W-C, Liu Z-W, Li C-J-Y, Xu R-J, Bao S-X, Li T-S, Jia P-S, Wu D-M, Gao N, Hyde KD, Wu G, Zhao Q (2025b) New and notable taxa of *Basidiomycota* on the Qinghai-Xizang Plateau and its surrounding areas. Fungal Diversity 133: 235–437. https://doi.org/10.1007/s13225-025-00558-x

Weiß M, Oberwinkler F (2001) Phylogenetic relationships in *Auriculariales* and related groups - hypotheses derived from nuclear ribosomal DNA sequences. Mycological Research 105: 403–415. https://doi.org/10.1017/S095375620100363X

White TJ, Bruns T, Lee S, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols: A Guide to Methods and Applications. Academic Press, New York, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wojewoda W (1981) Mała Flora Grzybów. Tom 2. Państwowe Wydawnictwo Naukowe, Warsaw, Krakow.

Wu F, Zhou LW, Yang ZL, Bau T, Li TH, Dai YC (2019) Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. Fungal Diversity 98: 1–76. https://doi.org/10.1007/s13225-019-00432-7

Wu F, Tohtirjap A, Fan LF, Zhou LW, Alvarenga RLM, Gibertoni TB, Dai YC (2021) Global diversity and updated phylogeny of *Auricularia* (*Auriculariales*, *Basidiomycota*). Journal of Fungi 7(11): 933. https://doi.org/10.3390/jof7110933

Yang Y, Xu Y, Wang L, Jiang QQ, Su JQ, Li R, Zhou HM, Zhao CL (2025) Multigene phylogeny of seven wood-inhabiting fungal orders in *Basidiomycota*, and proposal of

a new genus and thirteen new species. Mycosphere 16(1): 245–295. https://doi.org/10.5943/mycosphere/16/1/4

Zhao H, Cui YJ, Guan QX, Wang K, Zhuang L, Zeng GY, Wei YL, Wu F, Yuan HS (2025) Global fungal species diversity and distribution patterns within the order *Hymenochaetales* (*Agaricomycetes*, *Basidiomycota*). Mycosphere 16(1): 3257–3280. https://doi.org/10.5943/mycosphere/16/1/24

Zhou HM, Liu HG, Gates GM, Wu F, Dai YC, Cooper JA (2022) Phylogeny and diversity of the genus *Pseudohydnum* (*Auriculariales*, *Basidiomycota*). Journal of Fungi 8(7): 658. https://doi.org/10.3390/jof8070658

Zhou HM, Bau T, Si J (2023) Morphological and phylogenetic evidence reveal three new *Pseudohydnum* (*Auriculariales*, *Basidiomycota*) species from North China. Frontiers in Cellular and Infection Microbiology 13: 1139449. https://doi.org/10.3389/fcimb.2023.1139449

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Artificial Intelligence (AI) use

The authors accept full responsibility for the content of the manuscript, including the disclosure of any use of AI.
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Author contributions

Conceptualization: ZHT, HMZ, XZ. Data curation: HMZ, XZ, ZHT. Formal analysis: HMZ, XZ. Funding acquisition: YCD. Investigation: YCD, XZ, GYZ. Methodology: XZ, HMZ. Project administration: XZ, YCD. Resources: GYZ, YCD. Software: XZ. Validation: XZ. Visualization: HMZ, XZ. Writing – original draft: XZ. Writing – review and editing: XZ, YCD. All authors contributed to the article and approved the submitted version.

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Data availability

All of the data that support the findings of this study are available in the main text.